

## **FIGURE 1**

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG  
CTCTGTTGAGAATCATGCCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC  
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC  
AGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC  
CACC GGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT  
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG  
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT  
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT  
GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG  
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGATGTGTACC  
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT  
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG  
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG  
AACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT  
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATT  
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA  
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATACTCAGCATCTTTATCAC  
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT  
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTTCAGG  
AACCCCTGAAGTTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA  
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG  
TGTTACAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTC  
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG  
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTG  
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA  
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTT  
AGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT  
ATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAA

## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP  
GIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKEKGYPGIPPPELQIAFMASL  
ATHFSNQNSGIIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG  
NTVFSMYSYEMKGKSDTSSNHAFLKLAKGDEVWLRMGNGALHGDHQRFFSTFAGFLLFETK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **Motif name: Clq domain signature.**

amino acids 137-167

#### **Clq domain proteins.**

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

### **FIGURE 3**

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG  
CTCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT  
GGGCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTCTTCTGCTGGATGGTTTTT  
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGC  
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA  
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACTACATGTGGGACC  
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGG  
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA  
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA  
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT  
GGCCGGGCCGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG  
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGA  
CCAAGTGGATCCAGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCAC  
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA  
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAAC  
ACTCTGAGATATATAACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCC  
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA  
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA  
GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC  
ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGT  
GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCT  
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCTGTCTGGCCCAGC  
CACTGTGCCCTGGCACTGATTCTTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTC  
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAGCCAGATGATTTTCATTTTATGTGTGA  
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT  
TCTATACATAAAAGTTCCTACTTGTTAAA

## **FIGURE 4**

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDY  
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSL MPLWWNGSEPLW  
VTLTAKARKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA  
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRNLNVIIFSDHGMTDIFW  
MDKVIELNKYISLNDLQQVKDRGPVVSLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY  
KKGKFVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP  
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI  
LLFLLA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 100-104, 118-122, 341-345, 404-408

#### **N-myristoylation sites.**

amino acids 148-154, 365-371

#### **Amidation site.**

amino acids 343-347

## **FIGURE 5**

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACC**ATG**ACGCTCCTCC  
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG  
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCA  
GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG  
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG  
TGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC  
CTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT  
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG  
CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT  
CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCT  
GCGTGCTGCCCCGTTCAGTG**TGA**ACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGC  
TCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACT  
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC  
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA  
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA  
TCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT  
TAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

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## **FIGURE 6**

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL  
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKL  
AFAECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGGLPTPGAFAFHTEFIHVP  
VGCTCVLPRSV

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **Tyrosine kinase phosphorylation site.**

amino acids 112-121

#### **N-myristoylation sites.**

amino acids 32-38, 55-61, 133-139

#### **Leucine zipper pattern.**

amino acids 3-25

#### **Homologous region to IL-17.**

amino acids 99-195

## **FIGURE 7**

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAAC**ATG**CAGCTCGGCACTGGGCTCCTG  
CTGGCCGCCGTCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTCAACAGTGCAC  
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCA  
CTGCCACCCGGGTCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATA  
GGCTGCCCCGATATCCCCAGCCTGGGCCTGGGCCCCCTACGTATCCATCGCTTGCTGCCAGAC  
CAGCCTCTGCAACCATGAC**TGA**CGGCTGCCCTCCTCCAGGCCCCCGGACGCTCAGCCCCAC  
AGCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCCTCGAGACTGGCCAGCCCACC  
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGTCTAGGGAAGTCCTGCGTGGAGTC  
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGGCCCATCGTGCCTGCCGCCCCCTTCAGGTCCC  
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MLGTTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP  
LVTKMCHIGCPDIPSLGLGPYVSIACCQTS�CNHD

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 6-11 and 33-38

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 24-34 and 78-88



## FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAG  
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCT  
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG  
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG  
CTGGGCTCGGGCGGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTC  
GCGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG  
CCGCGATGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC  
TTCTGCGCCGCGTGGTTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA  
CAAAATGGCCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTT  
GTGAGAGTGAGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG  
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGG  
GCTTTGGAGGAATGGAGATGGGCAAACATCTGGTGCCTGCCAGATCTCTACCAGTGGTCTG  
ATGGAAGCAATTCAGTACCGAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG  
TGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA  
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA  
ATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT  
GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC  
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTA  
AAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA  
GAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAAATCTGGATC  
TGATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTTGAATCACAAAGGATCTGCAA  
GATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAGTAATTTTTATATGTCTATTATTTT  
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC  
CCAACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC  
GGGAGTATGTGTGTAGAACCAATTCCTTTTATTTCTTTTACCTTTTATAAGTTGTTATCTA  
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA  
GTGTTTGATAAAAAATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACAT  
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG  
TACCATAGAAAAAGTTTGTTTTCTCGAAATAATTCATCTTTTACGCTTCTCTGCTTTTGGTCA  
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTTATTAAGTGATATAAACCTCCTC  
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA  
TTATTTTATAGCTTAAAATTAACAGATTTTGTAAATGTAACCTTTGTTAATAGGTGCATAA  
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA  
CACGTTGCCATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC  
TTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC  
AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG  
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC  
ATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAATGGGTTGGAACCCATCAGTGATCG  
CATATTCATTGATGAGGGTTTGGCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC  
TAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTCTCTGGTCTTCA  
TATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTGTCTTCTGGGGGAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFRRVVSQGKVCFADEFKHPCKMAYFHELSSRVSFQEARLACE  
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDG  
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNICKYEPEINP  
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG  
RTKTSPNQSTLWISKSTRKESGMEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 214-235

#### **N-glycosylation sites.**

amino acids 86-89 and 255-258

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

#### **N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

## FIGURE 11

GGAGAAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCTGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG  
CCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCTGTGCGAGGCCGGCAGGTGG  
GCGTGAAGGGCACAGACCGCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCCAGCCGCCACTGGGCCCCTGACC  
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC  
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGAGGACT  
GCCTGGTCCCTCAACGTCTATAGCCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTTCATGGTATGGGTCCATG  
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGTGG  
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTACGACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA  
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTC  
ACAGAGCCATCACACAGAGTGGGGTTCATCACCACCCAGGGATCATCGACTCTCACCTTGGCCCCCTAGCTCAGA  
AAATCGCAAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
AAGAGCTGGTCTTGAAGAAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA  
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA  
GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT  
CAACACCCGTCTTGACCACTGTGGATGTGCCCCCTGAGATGATGCCACCCGTATAGATGAATACCTAGGAAGCA  
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCAGGAATTCATGGGTGACGTATTTCATCAATGTTCCACCGTCA  
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTTCTATGAGTTCCAGCATCGACCCAGTTCTTTTG  
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGTCTTTGTGTTCCGAGGTCCCTTCTCA  
TGGACGAGAGCTCCCGCCTGGCCTTTCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC  
AGTGGACCCACTTTGCCCCGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG  
AACAATATCTGGAGATCAACCCAGTGCCACGGGCCGACAGAAGTTCAAGGAGGCCCTGGATGCAGTTCTGGTCAG  
AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCACAGGAGACCTCTGAGGCC  
AGGCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCAGCACGGCAGCCCCCTCTC  
CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA  
ATGTCACAAGGCCGCTCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT  
CTTCGTGGTAGGTTCTAGCACATTCCTCTAGCTTCTGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC  
TGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT  
CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTACCCACACAGGATCGGGTGGGA  
CTGGAGTTAGGGGTGTTTGGTGTAGTGTAGTGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACTTGAAC  
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC  
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCCTGAC  
TAAGGCCTCAGACTAGGGCGGGAGGGTCTCCTCCTCTCTGCTGCCCAGTCTGGCCCCCTGCACAAGACAACAGA  
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCTCACCAATTCAGCCCCCTGACCCTCAGGACGCTGGATG  
CCAGCTCCCAGCCCCAGTGCCGGGTCTCCTCCTTCTTGGCTTGGGAGACAGTTTCTGGGGAGCTTCCAAG  
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGCGGCTATTGTACA  
GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGGTTTTTCAGATGGAAGTGAGAG  
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCCTGCCGCTCTGCCTGGGCTCCCACTTTGGCA  
GCACTTGAGGAGCCCTTCAACCCGCCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGGAGCCAGCT  
CCCTCAGCTTGGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGGGGCCAG  
AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGAGTGAGGGCCT  
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTTCTCGTGGGCCCTAGCTGCCTCCCCGCGGGGAGGGCTCGG  
GACCTGCAGCCCTCCATGCCTGACCCTCCCCCACCCCCCGTGGGCTCCTGTGCGGCCGAGCCTCCCCAAGGAG  
CGCCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACCACCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA  
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG  
GGACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT  
TGTAACACACCAATCAGCACCCTGTGTCTAGCTCAGTGTGTGTGAATGCACCAATCCACACTCTGTATCTGGCT  
ACTCTGGTGGGACTTGGAGAACCCTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCCT  
TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCCTGTCAAAACAGACCACTTGACTCTCTGTAAAT  
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC  
CCCTCGGGTCCCCCTCCACGCCGTGGAAGCTTTGTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGVKGTDRLVNVFLG  
IPFAQPPLGPDRFSAPHPAQWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC  
LVLNVYSPA EVPAGSGRPVMVWVHGGALITGAATSYDGSALAA YGDVVVVTVQYRLGVLGFF  
STGDEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIIISGLVLS PVAAGLF  
HRAITQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLOQKEGEELVLSKKLKNT  
IYPLTVDGTVPFKSPKELLKEKPFH SVPFMLGMVNNHEFSWLI PRGWGLLDTMEQMSREDMLA  
ISTPVLTSLDVPPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS  
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM  
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW  
HQKQKNRKAQEDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-27

#### **Transmembrane domain:**

amino acids 226-245

#### **N-glycosylation site.**

amino acids 105-109

#### **N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

#### **Carboxylesterases type-B serine active site.**

amino acids 216-232

## **FIGURE 13**

**CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAG**  
TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAA  
CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAGGAAGAACTGTTTCTCT  
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG  
ACAGAAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACCTCAGCGTG  
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATC  
TTTTGCAAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGAT  
CTGAAGGAGAACCTGCATTTAGATTTCTTGTGATTCTTCAAAGAAGGAACCAAGGTGGAAT  
TTTTGGAAGTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC  
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG  
AGGATCTA**TGA**GAAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG  
GTCTCATTTTTAAACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG  
CAGTAGTGC GTTCTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCA  
ATGAAGGATTTTTTTTTTAAATGTTATCTTGCTATTAAGTGGAATGAATGTTCCCAGGATGAG  
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAACACT  
TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG  
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT  
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG  
GAATAAAACACAAATGTTGAAAAATGTAAAATATATATACATAGATTCAAATCCTTATATAT  
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTTCTTTTTTAAGTACAGGTTCTTAGTGTTTT  
ACTATAACTGTCACTATGTATGTAAGTACATATATAAATAGTCATTTATAAATGACCGTAT  
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAAA

## **FIGURE 14**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSL  
EKYKGKVSLSVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFFPCNQFGESEPRPSKEVES  
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEP  
IEVIRPDIAALVRQVVIKKKEDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Glutathione peroxidases signature 2.**

amino acids 104-112

#### **Glutathione peroxidases.**

amino acids 57-82

## FIGURE 15

TGTCGCCTGGCCCTCGCCATGCAGACCCCGCGAGCGTCCCCTCCCCGCCCGGCCCTCCTGCTTCTGCTGCTGCTA  
CTGGGGGGGCGCCACGGCCTCTTCTGAGGAGCCGCCGCGCTTAGCGTGGCCCCAGGGACTACCTGAACCAC  
TATCCCGTGTGTTGTGGGCGAGCGGGCCCGACGCCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA  
GTCCTGCGGGTCAACAGGACGCTGTTTATGTTGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC  
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTCGGATGAAG  
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
GGTTCCAACGCCTTCAACCCGGTGTGCGCAACTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC  
GGTATGGCCCGCTGCCCCGTACGACCCCAAGCAGCÇAATGTTGCCCTCTTCTCTGACGGGATGCTCTTACAGCT  
ACTGTTACCGACTTCTAGCCATTGATGCTGTCATCTACCGCAGCCTCGGGGACAGGCCACCCTGCGCACCGTG  
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC  
TTCCGGGAGATTGCGATTGAGTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCCGAGTGTGCAAGAAC  
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCCTTCTGAAGGCGCGGCTCAACTGCTCTGTA  
CCCCGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAGCCTCGGGGGCGGGCCGTG  
GTCCTGGCCGTTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG  
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAG  
GTGCCTCGACCCCGGCCCGGGTGTGCGCAGCCCCCGGGATGCAGTACAATGCCCTCCAGCGCCTTGCCGGATGAC  
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG  
CGGACCCTGATGAGGCACCAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCCTGGGGCAACCAGACCGTT  
GTCTTCTGGGTTCTGAGGCGGGGACGGTCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT  
GGGCTCAGTGTCTTCTGGAGGAGTTTGAGACCTACCGGCCGACAGGTGTGGACGGCCCGGGTGGCGAGACA  
GGGCGAGCGGTGCTGAGCTTGGAGCTGGACGCAGCTTCCGGGGGCGCTGCTGGCTGCCTTCCCCCGCTGCGTGGTC  
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC  
GGGTGGGCCCCGACGGCTCCTGCATCTTCTCAGCCCGGGCACCAGAGCCGCTTTGAGCAGGACGTGTCCGGG  
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG  
TCGGTGAACCTGCTGGTAACGTGCTCGGTGGCGGCCTTCGTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGGC  
TGGTTCGTGGGCCTCCGTGAGCGGCGGGAGCTGGCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG  
GGCGAGGCGGTGCTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGGCGGAGGCGGT  
GGCGGTGGCGCCGGGGTTCCCCCGGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG  
CTGCAGGGCGGGCCCCACGACCTGGACTCGGGGTGCTGCCCCAGCCCCAGCAGACGCCGCTGCCCGAGAAGCGC  
CTGCCCCACTCCGACCCCGACCCCGACCCCTGGGCCCGCGCCTGGGACCACGGCCACCCCTGCTCCCGGCC  
TCCGCTTCATCCTCCCTCCTGCTGCTGGCGCCCGCCGGGCCCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC  
CCCGACGGCCGCTCTATGCTGCCCGGCCCGCGCGCCTCCACGGCGACTTCCCGCTCACCCCCACGCCAGC  
CCGGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCTTGGACCCAGCCTCAGCCGCCGATGGCCTCCCGCGG  
CCCTGGAGCCCCGCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCCTGCGC  
CGCACCCACAGTTCAACAGCGGCGAGGCCCGGCTGGGGACCGCCACCGCGGCTGCCACGCCCGCCGGGCACA  
GACTTGGCCACCTCCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGCCCTAGGCCGGGGGCCCCCGG  
ATGCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGACGGTGCCAGAACGCCGGGGCCCGGGGCAACTCCG  
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCGCGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAAACCAG  
CTCGCCCTCCCCCTACCCGGGGCCGACAGCAGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG  
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTTGCAGTTTTGGTTTTCTTTGCGGTTTTCTAACC  
AATTGCACAACTCCGTTCTCGGGTGGCGGCAGGCAGGGGAGGCTTGGACGCCGTTGGGAATGGGGGGCCACAG  
CTGCAGACCTAAGCCCCCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG  
TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG  
TGGGCGTGTGTGTCAAGTGGGCCACGCGTGCAGGCTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC  
CCCCCCTCTGTCAGAGGGAAGCGGGGACAATGCCGGGTTTTCAGGCAGGAGACACGAGGAGGGCCTGCCCGGA  
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAA  
ATACGGCCCCAGGGTGGTGAGAGAGTCCCATGCCACCCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA  
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCCTCCCCAGCCCCCTCCCCATCAAT  
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 16**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLGGAHGLFPEEPPPLSVAPRDYLNHYPVFVSGSGPGRLTPAEGA  
DDLNIQVRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG  
ECRNFKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALF  
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSFVYFFFREI  
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG  
VVSLLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPEDQVPR  
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDV  
GAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQ  
RLLSLELDAASGGLLAAPRCVVRVPVARCQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPG  
TRAAFEQDVSGASTSGLGDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW  
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGGGRRGGGGGGGAGVPPEALLA  
PLMQNGWAKATLLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLP  
SASSSLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRVVSAPTG  
PLDPASAADGLPRPWSPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG  
TDLAHLPPYGGADRTAPPVP

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domains:**

amino acids 318-339, 598-617

#### **N-glycosylation sites.**

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466

#### **Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

#### **N-myristoylation sites.**

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885



## **FIGURE 17**

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTCTCGGCCGGGACAGC  
AGAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCTGGGGTCG  
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGGCAACCTTTGCAGTCGCGTTGGCTGCTG  
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC  
ATTTATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT  
GCTTCTTTCTGGCGACAGTTCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCG  
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCTTCCCGCCCGCTATTT  
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT  
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCCTAGAGTTGGAGTCCAGGTTTTAGAC  
CGAAAAGATGGGTCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT  
GGAAATTAAATTCCAAGGGCAACATGTGGCCAAATCCCCATATATTTTAAAAGGGCCGGTTT  
ACCATGAGAACTGTGACTGTCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC  
CCTGAAACCATTTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAA  
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA  
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT  
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT  
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGT  
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG  
GAAACCATGGGCCGGGTAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTG  
GGAAAGCAAAAATTCCTACTGCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC  
TGTTTAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC  
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTTCAATTTTTTGATTTCTT  
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC  
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAG  
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACT  
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG  
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT  
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC  
TGAGGACGACCTCTTCCCTTGTAATTGCCATAGGAAAAAGACCAAAGATGAACTCTGAATATG  
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAAGAAGAATT  
TTTTTAAGTATTAATTCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA  
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTTAGAATTTTATAA  
TAAAACCACCTTTATTTTAAAGGAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKF  
TSSPGEKVFQVKVSAPEEQFTRVGVQVLDKDGSFIVRYRMYASYKNLKVVEIKFQGQHVAKS  
PYILKGPVYHENCDCPLQDSAALWREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR  
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNS  
NIHPIFSWCGSTDSDKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR  
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV  
AAYRLPYLLVGDSVVLKQDSIIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKK  
IAKAGQEFARNNLMGDDIFCYFVKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK  
KTKDEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **N-glycosylation sites.**

amino acids 302-306, 414-418

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

#### **Tyrosine kinase phosphorylation site.**

amino acids 341-348

#### **N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

#### **Endoplasmic reticulum targeting sequence.**

amino acids 499-504

## **FIGURE 19**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTTCGGTTCCGCATCCA  
GCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG  
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCC  
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCTAACTG  
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG  
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAA  
AAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT  
CAAGGCATTGATGACGGGGAGCCTTCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTC  
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT  
TATGGAGATGAAACCTGGGTAAATTTATCCCAAAGCATTTTGTGGAATATGATGGAACAAC  
CTCATTTTTCTGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG  
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC  
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT  
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG  
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG  
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA  
TCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA  
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAG  
CAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC  
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGGGAACT  
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCTATTCAACCTGGGCTCCAAGGTT  
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA  
GTTCTCACCCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT  
CCCCTGTCTCTCCTGGGTTTTCTCTGCTCTTTTATTGTTGGTGATCCTGGTTCTTTTCGGCCG  
TTCACGTCAATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG  
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG  
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGG  
TGTCCCGACACAGGTGTTACATCTGTGCTGTGAGGTGAGATGCCTCAGTTCTTGGAAGCT  
AGGTTCTCGCACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACACAGAGGAACAAGCCC  
CCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGA  
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTTCGCACCAC  
TCATCCTGCCACCCCAAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGA  
CGTTTTCTGTTGGAATTCTTAGTCTTGGCCTCGGACACCTTCATTTCGTTAGCTGGGGAGTG  
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACTCAGATCCACAGAGCCAGGATCAAG  
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCACCCCAACCCTGCACAGCCCTCATC  
CCCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT  
TGTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACGCTTGCACCTCGGGC  
CCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA  
GTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPP  
PLFSKVVIVLIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT  
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPHFVEYDGTTSFFVS  
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHT  
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208

## **FIGURE 21**

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATGG**CAAT  
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC  
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG  
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG  
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA  
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC  
AAATGCAACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC  
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA  
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC  
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG  
CACCACCGAGGGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG  
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT  
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC  
**ATAG**ACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC  
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL  
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA  
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSPVYIRTCHR  
PSCTTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 233-251

#### **N-glycosylation sites.**

amino acids 120-124, 174-178

#### **N-myristoylation sites.**

amino acids 15-21, 84-90

## FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG  
GAAAGGACAAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT  
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCTATGGCTGT  
CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT  
CCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT  
GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAG  
GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATAACGGGAATTTGCTCA  
CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTT  
CAAATTTTAATGGATGATCCCTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA  
TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAAAATATCAGAAAATACAGCTG  
AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA  
AACTACACGATCAGCCCCAATCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT  
GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT  
TAACCCTCACAGCGCTGGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC  
GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCAGGGCTCTGTATGAGACCCAGGC  
TCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG  
GAGTCAACGCGGAAGTATCCTATTCATTTTTTGTATGCCTCAGAAAATATTCGAACGACCTTT  
CAAATCAATCCTTTTTCTGGGGAAATCTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA  
TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCCTTCTGCAAGATGTAGGGTTT  
TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTTCCAAC  
TCTGTTGCTGAGAATTCTCCTGAGACGCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC  
TGGAGAAAATGGAAAGATGTTTGTCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT  
CTGTGGAGAATTTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG  
TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAACAT  
AACGGTCTCTGGTCTCCGACGTCAATGACAACGCCCCCGCCTTACCCAAACCTCCTACACCC  
TGTTTCGTCGCGAGACAACAGCCCCGCGCTGCACATCGGCAGCGTCAGCGCCACAGACAGA  
GACTCGGGACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCAAGACCCGACCTGCC  
CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTGCTGG  
ACTACGAGGCCCTGCAGGCTTTCGAGTTCGCGCTGGGCGCCACAGACCGCGGCTCCCCCGCG  
CTGAGCAGAGAGGCGCTGGTGCAGCTGCTGGTGGTGGACGCCAACGACAACCTCGCCCTTCGT  
GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCGGAGC  
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTG  
TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTTCGGTGTGTGGGCGCACAAATGGGGA  
GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCAGCCAAGCACAGGCTCGTGGTGTGTTG  
TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC  
GGCTTCTCCAGCCCTACCTGCCTCTCCCGAGGCGGCCCGGCCAGGCCCAGGCCCAGGCGAGGC  
CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCCTCCTCT  
CGGTGCTCCTGTTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCTCGGTGGGTGCG  
TGCTCGGTGCCCGAGGGTCCTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT  
GTCCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCGGGACCAGTGAGTTCAAGT  
TCTTGAAACCAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGTGAAGAAAAT  
TCCACCTTCCGAAATAGCTTTGGATTTAATATTCAGTAAAGTCTGTTTTTAGTTTCATATAC  
TTTTGGTGTGTACATAGCCATGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTAT  
TATGCAACTTCAAGCATTATTTTCAAGTAGTATACCCCTGTGGTTTTTACAATGTTTCATCAT  
TTTTTTGCATTAATAACAACCTGGGTTTAAATTTAATGAGTATTTTTTTCTAAATGATAGTGT  
AAGGTTTTAATCTTTTCCAACCTGCCAAGGAATTAATTACTATTATATCTCATTACAGAAAT  
CTGAGGTTTTGATTCATTTTCAAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTG  
TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTCTATATATT  
CGTGTTTGAAAACCATGTCAATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC  
TACTATGCTCATGACAAAATGAAACAAAGCATAATTGTGAGCAATACTGAACATCAATAATAC  
CCTTAGTTTATATACTTATTATTTTCTTAAAGCATGCTACTTTTACTTGGCCAATATTTT  
CTTATGTTAACTTTTGTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTTATA  
ATCTGCCTGAAAATGAATAAAAATAAAACATTTTGAAATGTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR  
GTRVVSDDNKQYLLLLDSHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVR  
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGGLNGIQNYTISPNSFFHINISGGD  
EGMIYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYE  
TQAPENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTTFQINPFSGEIFLRELLDYE  
LVNSYKINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND  
RDSGENGKMVCYIQENLPFLLKPSVENFYILITEGALDREIRAENITITVTDLGTPLRKTE  
HNITVLVSDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLASLV SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDFGSQPYLPLPEAAPAQAO  
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGA  
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 687-711

#### **N-glycosylation sites.**

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

#### **Glycosaminoglycan attachment site.**

amino acids 28-32

#### **Tyrosine kinase phosphorylation sites.**

amino acids 394-402, 578-585

#### **N-myristoylation sites.**

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,  
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

#### **Amidation site.**

amino acids 781-785

#### **Aminoacyl-transfer RNA synthetases class-II signature 1.**

amino acids 117-138

#### **Cadherins extracellular repeated domain signature.**

amino acids 121-132, 230-241, 335-346, 439-450, 549-560



[illegible][illegible]

## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234

><subunit 1 of 1, 507 aa, 1 stop

><MW: 56692, pI: 5.22, NX(S/T): 3

MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVVFQYIDLHQDEFVQTLKEWVAIESD  
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDQGQSLPIPPVILAELGSDPTK  
GTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD  
LPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY  
FMVEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY  
KAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGK  
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI  
RTVFGTEPDMIRDGSTIPIAKMFQÉIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF  
AAFFLEMAQLH

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

273-292

#### **N-glycosylation sites.**

amino acids 322-326, 382-386, 402-406

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 400-404

#### **N-myristoylation sites.**

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,  
351-357

#### **Cell attachment sequence.**

amino acids 140-143

#### **ArgE / dapE / ACY1 / CPG:**

amino acids 156-167

## **FIGURE 27**

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCTGGGAATTTAAGGGACCCACACTACCTTCC  
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCT**ATG**GGACCTGTGCGGTT  
GGGAATATTGCTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG  
AGGACGATGACACAGAACGCTTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG  
CTACAGGCGGAAGTGAAGTGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT  
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG  
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACAGCTGAGCGCAAGGGCTCA  
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG  
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT  
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC  
TTCCACCATCAGGAGCAGCCCCACAAAATTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC  
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAA  
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG  
ATGACCAAGACAGGAAGCCACCCCAAACCTTGACCGAGAAGATCTTT**TGA**CCCTTGCCTTTGAG  
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG  
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTTAGCTGTTCTCTCCCATCTAACC  
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG  
TCCTGCTCCTAGAGATGAACTCTATCCAGCCCCCTAATTGGCAGGTGTATGTGCTGACAGTA  
CTGAAAGCTTTCTCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC  
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCTTCCAAGGAAGA  
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA  
GCAAACCGTGAAGGAGAATGGGACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGG  
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT  
GCTCAACTTTCTATATCGCTATTAACTTTTTTCTTTTTTTCTA

## **FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL  
ELGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSLRYAKGQSQTMATLK  
GLVQKGVKVDLGIPLLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG  
HVLPAAETACLQETWTGKEITDGEEKTEGEEEEEEEEEEEEEGGDKMTKTGSHPKLDREDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 106-110

#### **N-myristoylation site.**

amino acids 115-121

#### **Amidation site.**

amino acids 70-74

## **FIGURE 29**

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT  
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTTGGACAATGAGGCTGGTCACAGCAGCACTG  
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCCTGTGCCCATGA  
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG  
GGAACATTGGCTGCAAGGTTGTTTCCTGATTGTAACAACCTACAGACAGAAGATCACCTCCTGG  
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT  
GGATCCAGATGCCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA  
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTAC  
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA  
GGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAATGG  
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG  
AACTACCAGGACTCACCAACCCTCCAGGCTCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA  
AACCAGGCAGAGAT**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC  
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA  
ATTAAAAAAAAAATCATCAA

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP  
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK  
KGKIQGQELSA YQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSKMDRFLNRFHL  
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation site.**

amino acids 169-173

#### **Tyrosine kinase phosphorylation site.**

amino acids 59-68

#### **N-myristoylation sites.**

amino acids 54-60, 83-89, 130-136

#### **Phosphatidylethanolamine signature.**

amino acids 113-157

## **FIGURE 31**

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTTCAGTCCCCTGGACTGTAGATAAAGA  
CCCTTTCTTGCCAGGTGCTGAGACAACCACACTATGGAGAGGCACTCCAGGAGACGCTGATGG  
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG  
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG  
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT  
GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT  
CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC  
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA  
CTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCCAATGTGT  
TTTCGTCTACATTTTCTTAGTGTCATTTTCACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG  
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG  
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCTCTCAAGCTGGTGCTGTGTAG  
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA  
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA  
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT  
ATGTTGCCAATATAACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAGACCTTGTAACA  
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC  
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA  
TCCAGTCTTTATATGTTGCCAATATAACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAG  
ACCTTGTAACAACAAAATAATTCTTGTGTTAAGTTAAATCATTTTTGTCTAATTGTAATGTG  
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACTGATATAAA  
ATAAAGAAAGAGTAAACTG

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## **FIGURE 32**

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL  
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY  
NTAFELNIND

### **Signal sequence:**

amino acids 1-17

### **N-myristoylation site.**

amino acids 10-16

### **Cell attachment sequence.**

amino acids 36-39

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL  
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY  
NTAFELNIND



## **FIGURE 33**

GCGAGGCTGCACCAGCGCCTGGCACCATGAGGACGCCTGGGCCTCTGCCCCTGCTGCTGCTG  
CTCCTGGCGGGAGCCCCCGCCGCGCGGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC  
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT  
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG  
CGGGACTTTGTGGCCTCGCCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCCTTGAAGGACAA  
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG  
ATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC  
TAAGGGAACTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT  
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA  
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCTACCCAGGAACCTCCTTTGAGCATAGA  
GTTAGCAACCATGCTTCTCATTCCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC  
ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAATA  
TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA  
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTTCTAACAC  
AGACTTTCTTCACTGTCTTTTCAATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTTACG  
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAATCAAATAAAGAATCTCTTC  
ACATGGA

1000 900 800 700 600 500 400 300 200 100 0

## **FIGURE 34**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY  
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLLDDCNALEY  
IPVTTVLPDRQR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site.**

amino acids 60-69

**N-myristoylation site.**

amino acids 16-22

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## **FIGURE 35**

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA  
CTTGACTCCCGCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTCAGAGATCCTGCA  
GCCGCCAGTCCCGGCCCTCTCCCGCCCCACACCCACCTCCTGGCTCTTCCTGTTTTTAC  
TCCTCCTTTTCATTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA  
AGCCGAGCGTGGAAGAATGGGGTTCTCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCC  
CGATTCAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA  
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAC  
ATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTGATAACTTGAACCTGC  
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA  
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA  
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC  
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT  
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTAT  
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT  
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG  
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG  
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTA  
AAACCTACAGTGAAGACAACCTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG  
AAAAGTATTGATTGAGAAAAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAC  
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT  
CCTACCTTGAAAACCTTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAT  
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA  
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA  
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT  
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAAATAAAGA  
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA  
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAA  
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAACACTTC  
TAATTCTGTGATTAAATTTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT  
TAACCTTTTACAAGTGGTTAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT  
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 36**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN  
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK  
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA  
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDET  
VSNTLTLTNGLERRTKTYSEDNFEELQYFPN FYALLKSIDSEKEAKEKETLITIMKTLIDFV  
KMMVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE  
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS  
KMRDFINKQADAYVEKGILDKEEA EAIKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

1990-1991	1991-1992	1992-1993	1993-1994	1994-1995	1995-1996	1996-1997	1997-1998	1998-1999	1999-2000	2000-2001	2001-2002	2002-2003	2003-2004	2004-2005	2005-2006	2006-2007	2007-2008	2008-2009	2009-2010	2010-2011	2011-2012	2012-2013	2013-2014	2014-2015	2015-2016	2016-2017	2017-2018	2018-2019	2019-2020	2020-2021	2021-2022	2022-2023	2023-2024	2024-2025	2025-2026	2026-2027	2027-2028	2028-2029	2029-2030	2030-2031	2031-2032	2032-2033	2033-2034	2034-2035	2035-2036	2036-2037	2037-2038	2038-2039	2039-2040	2040-2041	2041-2042	2042-2043	2043-2044	2044-2045	2045-2046	2046-2047	2047-2048	2048-2049	2049-2050	2050-2051	2051-2052	2052-2053	2053-2054	2054-2055	2055-2056	2056-2057	2057-2058	2058-2059	2059-2060	2060-2061	2061-2062	2062-2063	2063-2064	2064-2065	2065-2066	2066-2067	2067-2068	2068-2069	2069-2070	2070-2071	2071-2072	2072-2073	2073-2074	2074-2075	2075-2076	2076-2077	2077-2078	2078-2079	2079-2080	2080-2081	2081-2082	2082-2083	2083-2084	2084-2085	2085-2086	2086-2087	2087-2088	2088-2089	2089-2090	2090-2091	2091-2092	2092-2093	2093-2094	2094-2095	2095-2096	2096-2097	2097-2098	2098-2099	2099-2100	2100-2101	2101-2102	2102-2103	2103-2104	2104-2105	2105-2106	2106-2107	2107-2108	2108-2109	2109-2110	2110-2111	2111-2112	2112-2113	2113-2114	2114-2115	2115-2116	2116-2117	2117-2118	2118-2119	2119-2120	2120-2121	2121-2122	2122-2123	2123-2124	2124-2125	2125-2126	2126-2127	2127-2128	2128-2129	2129-2130	2130-2131	2131-2132	2132-2133	2133-2134	2134-2135	2135-2136	2136-2137	2137-2138	2138-2139	2139-2140	2140-2141	2141-2142	2142-2143	2143-2144	2144-2145	2145-2146	2146-2147	2147-2148	2148-2149	2149-2150	2150-2151	2151-2152	2152-2153	2153-2154	2154-2155	2155-2156	2156-2157	2157-2158	2158-2159	2159-2160	2160-2161	2161-2162	2162-2163	2163-2164	2164-2165	2165-2166	2166-2167	2167-2168	2168-2169	2169-2170	2170-2171	2171-2172	2172-2173	2173-2174	2174-2175	2175-2176	2176-2177	2177-2178	2178-2179	2179-2180	2180-2181	2181-2182	2182-2183	2183-2184	2184-2185	2185-2186	2186-2187	2187-2188	2188-2189	2189-2190	2190-2191	2191-2192	2192-2193	2193-2194	2194-2195	2195-2196	2196-2197	2197-2198	2198-2199	2199-2200	2200-2201	2201-2202	2202-2203	2203-2204	2204-2205	2205-2206	2206-2207	2207-2208	2208-2209	2209-2210	2210-2211	2211-2212	2212-2213	2213-2214	2214-2215	2215-2216	2216-2217	2217-2218	2218-2219	2219-2220	2220-2221	2221-2222	2222-2223	2223-2224	2224-2225	2225-2226	2226-2227	2227-2228	2228-2229	2229-2230	2230-2231	2231-2232	2232-2233	2233-2234	2234-2235	2235-2236	2236-2237	2237-2238	2238-2239	2239-2240	2240-2241	2241-2242	2242-2243	2243-2244	2244-2245	2245-2246	2246-2247	2247-2248	2248-2249	2249-2250	2250-2251	2251-2252	2252-2253	2253-2254	2254-2255	2255-2256	2256-2257	2257-2258	2258-2259	2259-2260	2260-2261	2261-2262	2262-
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[illegible]

## **FIGURE 38**

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR  
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL  
NVQFKPEIAQVGAKYQEAQGPGLLVVLFAVLRANPPANVTWIDQDGPVTVNTSDFLVLDAQN  
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGSPSRHPSLISSDSNNLKLNNVRLP  
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY  
RVSSVSSDEIWL

### **N-glycosylation sites:**

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,  
251-255, 280-284

### **Glycosaminoglycan attachment site:**

amino acids 23-27

### **Casein kinase II phosphorylation sites:**

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

### **N-myristoylation sites:**

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

## **FIGURE 39**

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCGGGGCG**ATGT**GGAGCGC  
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG  
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC  
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA  
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCG  
GCTCGGAGGGCGGGTGCCCCGCGGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG  
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA  
GGAGGTGAGTGCCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT  
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG  
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG  
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA  
GTGTGGAGCCCTCTGCAGGTCACGATGAACTC**TGAG**TGTGTGGATGGATGGGTGGATGGAGG  
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC  
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCGGGGCG**ATGT**GGAGCGC  
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG  
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC  
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA  
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCG  
GCTCGGAGGGCGGGTGCCCCGCGGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG  
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA  
GGAGGTGAGTGCCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT  
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG  
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG  
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA  
GTGTGGAGCCCTCTGCAGGTCACGATGAACTC**TGAG**TGTGTGGATGGATGGGTGGATGGAGG  
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC  
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

## **FIGURE 40**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPFVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS  
GSGQQSVTGVEASDDANSYWIRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPL  
SNNQEVSAFGEDGEGDDLDLWTVRCGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH  
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Glycosaminoglycan attachment site.**

amino acids 62-66

#### **N-myristoylation sites.**

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,  
91-97, 190-196

#### **Endoplasmic reticulum targeting sequence.**

amino acids 218-223



## **FIGURE 41**

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACCACAG  
ACGTGAGCCACTCCACCCAGCCTAAAACCTTCATCTTCTTTGGATGAGATGAACACTTTTAAC  
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT  
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAACTTACACA  
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT  
CGTCATC**ATG**TCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA  
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG  
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT  
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTTGGCCAAAAGTACTGCA  
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC  
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT  
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA  
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG  
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC  
ACGAGCCAAGTACCTCAAGAGACATGGCTTC**TAA**CATCTCAGATGAAACCCAAGACCATGAT  
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAAGTGGGAAT  
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAACCAAAAAAAAAAAAAA

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

## **FIGURE 42**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM  
PYLLKYQPMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE  
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA  
KYLKRHGF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **N-myristoylation sites.**

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

#### **Amidation site.**

amino acids 40-44

## **FIGURE 43**

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTTCTCAGGACCCTCGCCATGAAAG  
CCCTTATGCTGCTCACCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCAC  
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG  
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT  
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG  
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC  
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAG  
ACTCATTCCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT  
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG  
TTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT  
CCCTTCCCACCTTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT  
ATACTCTGCTGTCCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG  
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA  
AACCAGGCTCCCATATGTACCCCATCCCCCATACTCACCTCTTTCCATTTTGAGTAATAAA  
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAA

1000 900 800 700 600 500 400 300 200 100 0

## **FIGURE 44**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878

><subunit 1 of 1, 125 aa, 1 stop

><MW: 13821, pI: 8.60, NX(S/T): 2

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMVFSN  
LRCGTPEEPCQEAFNQTNRKLGITYNTTCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-18

#### **N-glycosylation sites.**

amino acids 77-81, 88-92

#### **N-myristoylation site.**

amino acids 84-90

#### **Ly-6 / u-PAR domain protein signature.**

amino acids 85-98

## FIGURE 45

ACGGGCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCA  
GTCGGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT  
ACCGCACCCAGGTTTCGGCCCGTAGGCGTCTGGCAGCCCGGCGCCATCTTCATCGAGCGCCAT  
GGCCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCATTTGTTC  
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA  
AAAGCTCTTACCCTCCACTATGACCGCTATAACACCTCCCGCAGGCTGGATCCCATCCCACA  
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTC  
AGAACAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA  
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT  
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC  
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCC  
TCGGCGGATTCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT  
TGTAAGTCTATAAGCTGTTCCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC  
CTCCATTTTCCCACCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT  
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGC  
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG  
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG  
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA  
TGGAGGCTCGGGCAGCTATTTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG  
GATATGGTGGTACCAGGAGACGATTAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT  
TTTGGATTTTTTCATCACTTTCTCTTTAGAAAAAAAGTACTACCTGTAAACAATTGGGAAAAG  
GGGATATTCAAAGTTCTGTGGTGTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAG  
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA  
TATTGCAGTTTTTTGAAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAC  
CTGTGATGCCCTAAGAAGCATTAAAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA  
AATTTAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA  
TTTGGTATTATATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA  
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTAGTGGTG  
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA  
GAAGGTTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTTCGT  
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC  
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

## **FIGURE 46**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPI P  
QLKCVGGTAGCDSYTPKVIQCQNKGWDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY  
VLRGSCGLEYNLDYTELGQLKESGKQHGFAFSFYKWSADSCNMSGELITIVVLLGIA  
FVVYKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS  
AFTGQQGYENSGPGFWTGLGTGGILGYLFSGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPL  
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 171-190

### **N-glycosylation site.**

amino acids 172-176

### **Glycosaminoglycan attachment sites.**

amino acids 244-248, 259-263, 331-335

### **Tyrosine kinase phosphorylation site.**

amino acids 98-106

### **N-myristoylation sites.**

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
270-276, 278-284, 312-318